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File: USPT

Jul 6, 1999

US-PAT-NO: 5919665

DOCUMENT-IDENTIFIER: US 5919665 A

TITLE: Vaccine for clostridium botulinum neurotoxin

DATE-ISSUED: July 6, 1999

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Williams; James A.	Madison	WI		

US-CL-CURRENT: 435/71.1; 435/252.3, 435/320.1, 530/350, 530/825, 536/23.4

CLAIMS:

I claim:

1. A soluble fusion protein comprising a non-toxin protein sequence and a portion of the Clostridium botulinum type A toxin, said portion of the Clostridium botulinum type A toxin comprising a portion of the sequence of SEQ ID NO:28.
2. The fusion protein of claim 1, wherein said portion of the Clostridium botulinum type A toxin sequence comprises SEQ ID NO:23.
3. The fusion protein of claim 1, wherein said non-toxin protein sequence comprises a poly-histidine tract.
4. The fusion protein of claim 3, which comprises SEQ ID NO:26.
5. The fusion protein of claim 1, wherein said fusion protein is substantially endotoxin-free.
6. A host cell containing a recombinant expression vector, said vector encoding a protein comprising at least a portion of a Clostridium botulinum type A toxin protein sequence of SEQ ID NO:28, and wherein said host cell is capable of expressing said protein as a soluble protein in said host cell at a level greater than or equal to 0.75% of the total cellular protein.
7. The host cell of claim 6, wherein said portion of a toxin comprises SEQ ID NO:23.
8. The host cell of claim 6, wherein said fusion protein comprises SEQ ID NO:26.
9. The host cell of claim 6, wherein said host cell is capable of expressing

said protein in said host cell at a level greater than or equal to 20% of the total cellular protein.

10. A soluble fusion protein, comprising at least a portion of Clostridium botulinum C fragment linked to a poly-histidine tag.

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UniProtKB/Swiss-Prot Release 47.8 of 30-Aug-2005

UniProtKB/TrEMBL Release 30.8 of 30-Aug-2005

updated search 9/05

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Search in UniProtKB/Swiss-Prot: There are matches to 9 out of 192799 entries

BXA1_CLOBO (P10845)

Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BoNT/A) (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-chain; Botulinum neurotoxin A heavy-chain]. {GENE: Name=botA; Synonyms=atx, bna} - Clostridium botulinum

BXA2_CLOBO (Q45894)

Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BoNT/A) (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-chain; Botulinum neurotoxin A heavy-chain]. {GENE: Name=botA; Synonyms=atx, bna} - Clostridium botulinum

BXB_CLOBO (P10844)

Botulinum neurotoxin type B precursor (EC 3.4.24.69) (BoNT/B) (Bontoxilysin B) [Contains: Botulinum neurotoxin B light chain; Botulinum neurotoxin B heavy chain]. {GENE: Name=botB} - Clostridium botulinum

BXC1_CLOBO (P18640)

Botulinum neurotoxin type C1 precursor (EC 3.4.24.69) (BoNT/C1) (Bontoxilysin C1) [Contains: Botulinum neurotoxin C1 light chain; Botulinum neurotoxin C1 heavy chain]. - Clostridium botulinum

BXD_CLOBO (P19321)

Botulinum neurotoxin type D precursor (EC 3.4.24.69) (BoNT/D) (Bontoxilysin D) [Contains: Botulinum neurotoxin D light chain; Botulinum neurotoxin D heavy chain]. {GENE: Name=botD} - Clostridium botulinum

BXE_CLOBO (Q00496)

Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BoNT/E) (Bontoxilysin E) [Contains: Botulinum neurotoxin E light chain; Botulinum neurotoxin E heavy chain]. - Clostridium botulinum

BXE_CLOBU (P30995)

Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BoNT/E) (Bontoxilysin E) [Contains: Botulinum neurotoxin E light chain; Botulinum neurotoxin E heavy chain]. - Clostridium butyricum

BXF CLOBO (P30996)

Botulinum neurotoxin type F precursor (EC 3.4.24.69) (BoNT/F) (Bontoxilysin F) [Contains: Botulinum neurotoxin F light chain; Botulinum neurotoxin F heavy chain]. {GENE: Name=botF} - Clostridium botulinum

BXG CLOBO (Q60393)

Botulinum neurotoxin type G precursor (EC 3.4.24.69) (BoNT/G) (Bontoxilysin G) [Contains: Botulinum neurotoxin G light chain; Botulinum neurotoxin G heavy chain]. {GENE: Name=botG} - Clostridium botulinum

Search in UniProtKB/TrEMBL: There are matches to 1 out of 1973644 entries

Q9R540 CLOBO

Neurotoxin heavy chain 18 kDa fragment (Fragment) - Clostridium botulinum

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sp P10845 Botulinum neurotoxin type A precursor (EC 3.4.24.69) 1295
 BXA1_CLOBO (BoNT/A) AA
 (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin align
 A light-chain; Botulinum neurotoxin A heavy-chain] [botA]
 [Clostridium botulinum]

Score = 862 bits (2227), Expect = 0.0

Identities = 422/423 (99%), Positives = 422/423 (99%), Gaps = 1/423 (0%)

Query: 1 INTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
 INTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
 Sbjct: 873 INTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 932

Query: 61 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI 120
 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI
 Sbjct: 933 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI 992

Query: 121 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI
 Sbjct: 993 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 1052

Query: 181 MFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYDKPYYM 240
 MFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYDKPYYM
 Sbjct: 1053 MFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYDKPYYM 1112

Query: 241 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI 300
 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI
 Sbjct: 1113 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI 1172

Query: 301 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQ-VVMKSKNDQGITN 359
 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQ VVMKSKNDQGITN
 Sbjct: 1173 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKNDQGITN 1232

Query: 360 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYRQIERSSRTLGC SWEFIPVDDGWGE 419
 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYRQIERSSRTLGC SWEFIPVDDGWGE
 Sbjct: 1233 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYRQIERSSRTLGC SWEFIPVDDGWGE 1292

Query: 420 RPL 422
 RPL
 Sbjct: 1293 RPL 1295

tr Q7B8V4 BoNT/A (Neurotoxin BoNT) [bont/a] [Clostridium 1296
 Q7B8V4_CLOBO botulinum] AA
 align

Score = 862 bits (2227), Expect = 0.0

Identities = 422/423 (99%), Positives = 422/423 (99%), Gaps = 1/423 (0%)

Query: 1 INTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
 INTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
 Sbjct: 874 INTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 933

Query: 61 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI 120
 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI
 Sbjct: 934 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI 993

Query: 121 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI
 Sbjct: 994 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 1053

Query: 181 MFKLDGCRDTHRYIWIKEYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQYDKPYM 240
 MFKLDGCRDTHRYIWIKEYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQYDKPYM
 Sbjct: 1054 MFKLDGCRDTHRYIWIKEYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQYDKPYM 1113

Query: 241 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIKKYASGNKDNI 300
 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIKKYASGNKDNI
 Sbjct: 1114 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIKKYASGNKDNI 1173

Query: 301 VRNNDRVYINVVVKKEYRLATNASQAGVEKILSALEIPDVGNLSQ-VVMKSKNDQGITN 359
 VRNNDRVYINVVVKKEYRLATNASQAGVEKILSALEIPDVGNLSQ VVMKSKNDQGITN
 Sbjct: 1174 VRNNDRVYINVVVKKEYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKNDQGITN 1233

Query: 360 KCKMNLQDNNGNDIGFIGFHQFNNAKLVASNWNRYNRQIERSSRTLGCSEWFIPVDDGWGE 419
 KCKMNLQDNNGNDIGFIGFHQFNNAKLVASNWNRYNRQIERSSRTLGCSEWFIPVDDGWGE
 Sbjct: 1234 KCKMNLQDNNGNDIGFIGFHQFNNAKLVASNWNRYNRQIERSSRTLGCSEWFIPVDDGWGE 1293

Query: 420 RPL 422
 RPL
 Sbjct: 1294 RPL 1296

sp Q45894 Botulinum neurotoxin type A precursor (EC 3.4.24.69) 1295
 BXA2_CLOBO (BoNT/A) AA
 (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin align
 A light-chain; Botulinum neurotoxin A heavy-chain] [botA]
 [Clostridium botulinum]

Score = 759 bits (1960), Expect = 0.0
 Identities = 367/423 (86%), Positives = 396/423 (92%), Gaps = 1/423 (0%)

Query: 1 INTSILNLRYESNHLIDLRSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
 +NTSIL++ Y+ + LIDLSRY +KINIG +V +D IDKNQI+L NLESS IEVILKNAIV
 Sbjct: 873 VNTSILSIVYKKDDLIDLRSYGAKINIGDRVYYSIDKNQIKLINLESSTIEVILKNAIV 932

Query: 61 YNSMYENFSTSFWRIPKYFNSISLNNEYTIINC MENNSGWKVSLNYGEIIWTLQDTQEI 120
 YNSMYENFSTSFWI+IPKYF+ I+LNNEYTIINC+ENNSGWKVSLNYGEIIWTLQD ++
 Sbjct: 933 YNSMYENFSTSFWIKIPKYFSKINLNNEYTIINCIENNSGWKVSLNYGEIIWTLQDNKQN 992

Query: 121 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
 QRVVFYKYSQM+NISDYINRWIFVTITNNRL SKIYINGRLIDQKPISNLGNIHASN I
 Sbjct: 993 IQRVVFYKYSQMVNISDYINRWIFVTITNNRLTKSKIYINGRLIDQKPISNLGNIHASNKI 1052

Query: 181 MFKLDGCRDTHRYIWIKEYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQYDKPYM 240
 MFKLDGCRD RYI IKYFNLFDKELNEKEIKDLYD+QSN SGILKDFWG+YLQYDKPYM
 Sbjct: 1053 MFKLDGCRDPRRYIMIKYFNLFDKELNEKEIKDLYDSQSN SGILKDFWGNLYLYQYDKPYM 1112

Query: 241 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIKKYASGNKDNI 300
 LNL+DPNKYVDVNN+GIRGYMYLKGPRGSV+TTNIYLN+LY GTKFIKKYASGN+DNI
 Sbjct: 1113 LNLFDPNKYVDVNNIGIRGYMYLKGPRGSVVTTNIYLNSTLYEGTKFIKKYASGNEDNI 1172

Query: 301 VRNNDRVYINVVVKKEYRLATNASQAGVEKILSALEIPDVGNLSQ-VVMKSKNDQGITN 359
 VRNNDRVYINVVVKKEYRLATNASQAGVEKILSALEIPDVGNLSQ VVMKSK+DQGI N

Sbjct: 1173 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKDDQGIRN 1232

Query: 360 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYNQIERSSRTLGCSEFIPVDDGWGE 419
KCKMNLQDNNNGNDIGFIGFH ++NIAKLVASNWNRYNQ+ ++SRT GCSWEFIPVDDGWGE

Sbjct: 1233 KCKMNLQDNNNGNDIGFIGFHLVDNIAKLVASNWNRYNQVGKASRTFGCSWEFIPVDDGWGE 1292

Query: 420 RPL 422
L

Sbjct: 1293 SSL 1295

tr Q58GH1 Type A2 botulinum neurotoxin [Clostridium botulinum] 1296 AA
Q58GH1_CLOBO

align

Score = 759 bits (1960), Expect = 0.0

Identities = 367/423 (86%), Positives = 396/423 (92%), Gaps = 1/423 (0%)

Query: 1 INTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
+NTSIL++ Y+ + LIDLRLRY +KINIG +V +D IDKNQI+L NLESS IEVILKNAIV

Sbjct: 874 VNTSILSIVYKKDDLIDLRLRYGAKINIGDRVYYSIDKNQIKLINLESSTIEVILKNAIV 933

Query: 61 YNSMYENFSTSFWRIPKYFNSISLNNEYTIINC MENNSGWKVS LNYGEIIWTLQDTQEI 120
YNSMYENFSTSFWRIPKYF+ I+LNNEYTIINC+ENNSGWKVS LNYGEIIWTLQD ++

Sbjct: 934 YNSMYENFSTSFWRIPKYFNSISLNNEYTIINC IENNSGWKVS LNYGEIIWTLQDNKQN 993

Query: 121 KQRVVFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
QRVVFKYSQM+NISDYINRWIFVTITNNRL SKIYINGRLIDQKPISNLGNIHASN I

Sbjct: 994 IQRVVFKYSQMVNISDYINRWIFVTITNNRLTKSKIYINGRLIDQKPISNLGNIHASNKI 1053

Query: 181 MFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDQSN SGILKDFWGDYLYQDKPYM 240
MFKLDGCRD RYI IKYFNLFDKELNEKEIKDLYD+QSN SGILKDFWG+YLQDKPYM

Sbjct: 1054 MFKLDGCRDPRRYIMIKYFNLFDKELNEKEIKDLYDQSN SGILKDFWGNLYQDKPYM 1113

Query: 241 LNLDPN KYVDVNNVGIRGYMYLKGPRGSMVT TTIYLNSSLYRGTKFIKKYASGNKDNI 300
LNL+DPN KYVDVNN+GIRGYMYLKGPRGSM+TTIYLNSSLY+LY GTKFIKKYASGN+DNI

Sbjct: 1114 LNLDPN KYVDVNNVGIRGYMYLKGPRGSMVT TTIYLNSSLYEGTKFIKKYASGNEDNI 1173

Query: 301 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQ-VVMKSKNDQGIRN 359
VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQ VVMKSK+DQGI N

Sbjct: 1174 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKDDQGIRN 1233

Query: 360 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYNQIERSSRTLGCSEFIPVDDGWGE 419
KCKMNLQDNNNGNDIGFIGFH ++NIAKLVASNWNRYNQ+ ++SRT GCSWEFIPVDDGWGE

Sbjct: 1234 KCKMNLQDNNNGNDIGFIGFHLVDNIAKLVASNWNRYNQVGKASRTFGCSWEFIPVDDGWGE 1293

Query: 420 RPL 422
L

Sbjct: 1294 SSL 1295

tr Q57236 BoNT/F (Neurotoxin type F) [bont/f] [Clostridium 1278
Q57236_CLOBO botulinum] AA
align

Score = 417 bits (1073), Expect = e-115

Identities = 211/423 (49%), Positives = 285/423 (66%), Gaps = 18/423 (4%)

```

Query: 2      NTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVY 61
              + SIL++RYE+N ID+S Y S I+I V ++NQ +++ + S++ + N I+Y
Sbjct: 868    DNSILDMRYENNKFIDISGYGSNISINGDVYIYSTNRNQFGIYSSKPSEVNIAQNNDIY 927

Query: 62     NSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENN-SGWKVS LNYGEIIWTLQDTQEI 120
              N Y+NFS SFW+RIPKYFN ++LNNEYTII+C+ NN SGWK+SLNY +IIWTLQDT
Sbjct: 928    NGRYQNFSISFWVRIPKYFNKVN LNNEYTIIDCIRNNNSGWKISLNYNKIIWTLQDTAGN 987

Query: 121     KQRVVF KYSQMINISDYINRWIFVTITNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
              Q++VF Y+QMI+ISDYIN+WIFVTITNRL NS+IYING LID+K ISNLG+IH S+NI
Sbjct: 988    NQKL VFN Y TQ M I S D Y I N K W I F V T I T N R L G N S R I Y I N G N L I D E K S I S N L G D I H V S D N I 1047

Query: 181     MFKLDGCRDTHRYIWI KYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQDKPYM 240
              +FK+ GC DT RY+ I+YF +FD EL + EI+ LY ++ + ILKDFWG+YL Y+K YY+
Sbjct: 1048   LFKIVGCNDT-RYVGIRYFKVFDTEL GKTEIETLYSDEPDPSILKDFWGN YLLYNKRYYL 1106

Query: 241     LNL YDPNKYVDVNNVGIRGYMYLKGPRGSMVT T NI YL NSSLYRGTKFIIKKYAS---GNK 297
              LNL +K + N+ ++ + RG NI+ N+ LY G + II+K S N
Sbjct: 1107   LNL LRTDKSITQNS----NFLNINQQRGVYQKPNIFSNTRL YTGVEVIIRKNGSTDISNT 1162

Query: 298     DNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGN-LSQVVMKSKNDQG 356
              DN VR ND YINVV ++ EYRL + S A EKI+ + + N L Q+++
Sbjct: 1163   DNFVRKNDLAYINVVDRDVEYRLYADISI AKPEKIIKLIRTSNNSNLSLQGIIVM----DS 1218

Query: 357     ITNKCKMNLQDNNGNDIGFIGFHQFN N IAKLVASNWYNRQIERSSRTLGC SWEFIPVDDG 416
              I N C MN Q+NNG +IG +GFH N LVAS+WY I +++ + GC W FI + G
Sbjct: 1219   IGNNCTMNFQNNNGGNIGLLGFHSNN---LVASSWYNNIRKNTSSNGCFWFSFISKEHG 1274

Query: 417     WGE 419
              W E
Sbjct: 1275   WQE 1277

```

```

tr   Q45851      Neurotoxin type F [bont /f] [Clostridium      1268 AA
      Q45851_9CLOT      baratii]      align

```

Score = 416 bits (1070), Expect = e-115

Identities = 214/424 (50%), Positives = 281/424 (65%), Gaps = 18/424 (4%)

```

Query: 1      INTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
              I++SILN++YE+N ID S Y S I+I + ++NQ +++ S++ + N I+
Sbjct: 858    IDSSILNMKYENNR FIDSSGYGSNISINGDIYIYSTNRNQFGIYSSRLSEVNITQNNTII 917

Query: 61     YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENN-SGWKVS LNYGEIIWTLQDTQE 119
              YNS Y+NFS SFW+RIPKY N +LNNEYTIINCM NN SGWK+SLNY IIWTLQDT
Sbjct: 918    YNSRYQNFSVSFWVRIPKYNNLKNLNNEYTIINCMRNNNSGWKISLNYNNIIWTLQDTTG 977

Query: 120     IKQRVVF KYSQMINISDYINRWIFVTITNRLNNSKIYINGRLIDQKPISNLGNIHASNN 179
              Q++VF Y+QMI+ISDYIN+W FVTITNRL +SK+YING L DQK I NLGNIH +N
Sbjct: 978    NNQKL VFN Y TQ M I S D Y I N K W T F V T I T N R L G H S K L Y I N G N L T D Q K S I L N L G N I H V D D N 1037

Query: 180     IMFKLDGCRDTHRYIWI KYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQDKPY 239
              I+FK+ GC DT RY+ I+YF +F+ EL++ EI+ LY ++ +S ILKDFWG+YL Y+K YY

```


Sbjct: 1038 ILFKIVGCNDT-RYVGIRYFKIFNMELDKTEIETLYHSEPDSTILKDFWGNLYLLYNKKYY 1096

Query: 240 MLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYAS---GN 296
+LNL PN V N+ + + RG TNI+ N+ LY G + II+K S N

Sbjct: 1097 LLNLLKPNMSVTKNS---DILNINRQGIYSKTNIFSNARLYTGVEVIIRKVGSTDTSN 1152

Query: 297 KDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVG-NLSQVVMKSKNDQ 355
DN VR ND VYINVV N EY+L + S + VEK + I + N +Q+++

Sbjct: 1153 TDNFVRKNDTVYINVVDGNSEYQLYADVSTSAVEKTIKLRRISNSNYNSNQMIIM---D 1208

Query: 356 GITNKCKMNLQDNNNDIGFIGFHQFNNAKLVASNWNRYRQIERSSRTLGCSEFIPVDD 415
I + C MN + NNGNDIG +GFH N LVAS+WY + I ++R GC W FI +

Sbjct: 1209 SIGDNCTMNFKTNNNDIGLLGFHLNN---LVASSWYKYNIRNNTRNNGCFWSFISKEH 1264

Query: 416 GWGE 419
GW E

Sbjct: 1265 GWQE 1268

tr Q9K395 Type E botulinum toxin [bont/E] [Clostridium butyricum] 1251 AA
Q9K395_CLOBU align

Score = 379 bits (974), Expect = e-104

Identities = 200/431 (46%), Positives = 273/431 (62%), Gaps = 40/431 (9%)

Query: 2 NTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVY 61
++S+LN+RY+++ +D S Y S INI ++ P +KNQ +FN + S++ + + I+Y

Sbjct: 849 SSSVLNMRKYKNDKYVDTSGYDSNININGEIFIYPTNKNQFTIFNSKPSEVNISQNDYIIY 908

Query: 62 NSMYENFSTSFWIRIPKYFNSI-SLNNEYTIINC-M-ENNSGWKVSLNYGEIIWTLQDTQE 119
++ Y+NFS SEW+RIP Y N I ++NNEYTIINC-M-ENNSGWKVSLN+ EIIWTLQD

Sbjct: 909 DNKYKNFSISFWVRIPNYDNKIVNINNEYTIINCMRDNNSGWKVSLNHNEIIWTLQDNAR 968

Query: 120 IKQRVVFKYSQMINISDYINRWIFVTITNRLNNSKIYINGRLIDQKPISNLGNIHASNN 179
I Q++VFKY ISDYIN+WIFVTITN+RL +SK+YING LIDQK I NLGNIH S+N

Sbjct: 969 INQKLVFKYGNANGISDYINKWIFVTITNDRLGDSKLYINGHLIDQKSILNLGNIHVSDN 1028

Query: 180 IMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNSGILKDFWGDYLYDKPYY 239
I+FK+ C T RYI I+YFN+FDKEL+E EI+ LY N+ N+ ILKDFWG+YL YDK YY

Sbjct: 1029 ILFKIVNCSYT-RYIGIRYFNIFDKELDETEIQTLYSNEPNTNILKDFWGNLYLLYDKGY 1087

Query: 240 MLNLYDPNKYVD-----VNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKK 291
+LN+ PN ++D +NN+ + I L + LY G K I++

Sbjct: 1088 LLNVLPNNFIDRRKDSTLSINNI-----RSTILLANRLYSGIKVKIQR 1131

Query: 292 Y-ASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGN-LSQVVM 349
S D VR ND+VYIN + + Y L + + EK + + GN +QVV+

Sbjct: 1132 VNDSSSTNDRFVRKNDQVYINYISNSSSYSLYADTNTTDEKTIKS---SSSGNRFNQVVV 1188

Query: 350 KSKNDQGKITNKCKMNLQDNNNDIGFIGFHQFNNAKLVASNWNRYRQIERSSRTLGCSE 409
+ + N C MN ++NNGN+IG +GF +VAS WY + + + GC W

Sbjct: 1189 MN----SVGNCTMNFKNNGNIGLLGF----KADTVVASTWYYTHMRDHTNSNGCFWN 1240

Query: 410 FIPVDDGWGER 420
FI + GW E+

Sbjct: 1241 FISEEHGWQEK 1251

tr Q9ZAJ5 BonT protein [bonT] [Clostridium 1280 AA
Q9ZAJ5_CLOBO botulinum] align

Score = 379 bits (973), Expect = e-104

Identities = 196/426 (46%), Positives = 276/426 (64%), Gaps = 21/426 (4%)

Query: 2 NTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVY 61
++SIL++RYE+N ID+S Y S I+I V ++NQ +++ S++ + N I+Y
Sbjct: 868 DSSILDMRYENNKFIDISGYGSNISINGNVYIYSTNRNQFGIYSGRLSEVNIAQNNDIIY 927

Query: 62 NSMYENFSTSFWIRIPKYFNSISLNNEYTIINCM-ENNSGWKVS LNY---GEIIWTLQDT 117
NS Y+NFS SFW+ IPK++ ++ N EYTIINCM NNSGWK+SL EIIWTLQDT
Sbjct: 928 NSRYQNFSISFWVTIPKHYRPMNRNREYTIINCMGNNSGWKISLRTIRDCEIIWTLQDT 987

Query: 118 QEIKQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHAS 177
K++++F+Y ++ +ISDYIN+WIFVTITNNRL NS+IYING LI +K ISNLG+IH S
Sbjct: 988 SGNKEKLIFRYEELASISDYINKWIFVTITNNRLGNSRIYINGNLIVEKSISNLGDIHVS 1047

Query: 178 NNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQYDKP 237
+NI+FK+ GC D Y+ I+YF +F+ EL++ EI+ LY N+ + ILKD+WG+YL Y+K
Sbjct: 1048 DNILFKIVGC-DDETYVGIRYFKVFNTELDKTEIETLYSNEPDPSILKDYWGNYLLYNKK 1106

Query: 238 YYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYAS--- 294
YY+ NL +KY+ N+ G + + RG +++LN LY G + II+K A
Sbjct: 1107 YYLFNLLRKDKYITRNS----GILNINQQRGVTGGISVFLNYKLYEGVEVIIRKNAPIDI 1162

Query: 295 GNKDNIVRNNDRVYINVVVNKEYRLATNASQAGVEKILSALEIPDVG-NLSQVVMKSKN 353
N DN VR ND YINVV EYRL + S EKI+ + + +L Q+++
Sbjct: 1163 SNTDNFVRKNLDLAYINVVDHGVEYRLYADISITKSEKIIKLIRTSNPNDSLGQIIIVM--- 1219

Query: 354 DQGITNKCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYQIERSSRTLGCSEWFIPV 413
I N C MN Q+N+G++IG +GFH + LVAS+WY I R++ + GC W FI
Sbjct: 1220 -DSIGNNCTMNFQNNDGSGNIGLLGFHSDD----LVASSWYNNHIRRNTSSNGCFWSFISK 1274

Query: 414 DDGWGE 419
+ GW E
Sbjct: 1275 EHWKE 1280

sp P30996 Botulinum neurotoxin type F precursor (EC 3.4.24.69) 1274
BXF_CLOBO (BoNT/F) AA
(Bontoxilysin F) [Contains: Botulinum neurotoxin F light align
chain; Botulinum neurotoxin F heavy chain] [botF]
[Clostridium botulinum]

Score = 377 bits (968), Expect = e-103

Identities = 197/425 (46%), Positives = 279/425 (65%), Gaps = 24/425 (5%)

Query: 2 NTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVY 61
++SIL++RYE+N ID+S Y S I+I V ++NQ ++N S++ + N I+Y
Sbjct: 867 DSSILDMRYENNKFIDISGYGSNISINGNVYIYSTNRNQFGIYNSRLSEVNIAQNNDIIY 926

Query: 62 NSMYENFSTSFWIRIPKYFNSISLNN EYTIINCM-ENNSGWKVSLNYG---EIIWTLQDT 117
NS Y+NFS SFW+RIPK++ ++ N EYTIINCM NNSGWK+SL EIIWTLQDT
Sbjct: 927 NSRYQNFSISFWVRIPKHYKPMNHNREYTIINCMGNNNSGWKISLRTVRDCEIIWTLQDT 986

Query: 118 QEIKQRVVFQYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHAS 177
K+ ++F+Y ++ IS+YIN+WIFVTITNNRL NS+IYING LI +K ISNLG+IH S
Sbjct: 987 SGNKENLIFRYEELNRISNYINKWIFVTITNNRLGNSRIYINGNLIVEKSISNLGDIHVS 1046

Query: 178 NNIMFKLDGCRDTHRYIWIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYDKP 237
+NI+FK+ GC D Y+ I+YF +F+ EL++ EI+ LY N+ + ILK++WG+YL Y+K
Sbjct: 1047 DNILFKIVGC-DETYVGIRYFKVFNTELDKTEIETLYSNEPDPSILKNYWGNYLLYNKK 1105

Query: 238 YYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYAS--- 294
YY+ NL +KY+ +N+ G + + RG V +++LN LY G + II+K
Sbjct: 1106 YYLFNLLRKDKYITLNS---GILNINQQRG-VTEGSVFLNYKLYEGVEVIIRKNGPIDI 1160

Query: 295 GNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKND 354
N DN VR ND YINVV + EYRL + +++ EKI+ + D +L Q+++
Sbjct: 1161 SNTDNFVRKNDLAYINVVDRGVEYRLYAD-TKSEKEKIIRTSNLND--SLGQIIVM---- 1213

Query: 355 QGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSEWIFIPVD 414
I N C MN Q+NNG++IG +GFH N LVAS+WY I R++ + GC W I +
Sbjct: 1214 DSIGNNCTMNFQNNNGSNIGLLGFHSNN---LVASSWYNNIRNTSSNGCFWSSISKE 1269

Query: 415 DGWGE 419
+GW E
Sbjct: 1270 NGWKE 1274

Db AC	Description	Score	E-value
<input checked="" type="checkbox"/> sp P10845	BXA1_CLOBO Botulinum neurotoxin type A precursor (EC 3...	862	0.0
<input checked="" type="checkbox"/> tr Q7B8V4	_CLOBO BoNT/A (Neurotoxin BoNT) [bont/a] [Clostridium b...	862	0.0
<input checked="" type="checkbox"/> sp Q45894	BXA2_CLOBO Botulinum neurotoxin type A precursor (EC 3...	759	0.0
<input checked="" type="checkbox"/> tr Q58GH1	_CLOBO Type A2 botulinum neurotoxin [Clostridium botuli...	759	0.0

CLUSTAL W (1.82) multiple sequence alignment

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sp|P10845|BXA1_CLOBO      -PFVNKQFNYPKDPVNGVDIAYIKIPNVGQMQPVKAFKIHNKIWPVPERDT
tr|Q7B8V4|Q7B8V4_CLOBO  MPFVNKQFNYPKDPVNGVDIAYIKIPNAGQMQPVKAFKIHNKIWPVPERDT
sp|Q45894|BXA2_CLOBO      -PFVNKQFNYPKDPVNGVDIAYIKIPNAGQMQPVKAFKIHNKIWPVPERDT
tr|Q58GH1|Q58GH1_CLOBO  MPFVNKQFNYPKDPVNGVDIAYIKIPNAGQMQPVKAFKIHNKIWPVPERDT
                          *****

sp|P10845|BXA1_CLOBO      FTNPEEGDLNPPPEAKQVPVSYDSTYLSTDNEKDNLYKGVTKLFERIYS
tr|Q7B8V4|Q7B8V4_CLOBO  FTNPEEGDLNPPPEAKQVPVSYDSTYLSTDNEKDNLYKGVTKLFERIYS
sp|Q45894|BXA2_CLOBO      FTNPEEGDLNPPPEAKQVPVSYDSTYLSTDNEKDNLYKGVTKLFERIYS
tr|Q58GH1|Q58GH1_CLOBO  FTNPEEGDLNPPPEAKQVPVSYDSTYLSTDNEKDNLYKGVTKLFERIYS
                          *****

sp|P10845|BXA1_CLOBO      TDLGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDGSYRSEELN
tr|Q7B8V4|Q7B8V4_CLOBO  TDLGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDGSYRSEELN
sp|Q45894|BXA2_CLOBO      TDLGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDGSYRSEELN
tr|Q58GH1|Q58GH1_CLOBO  TDLGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDGSYRSEELN
                          *****

sp|P10845|BXA1_CLOBO      LVIIGPSADIIQFECKSFGHEVLNLTNRNGYGSTQYIRFSPDFTFGFEESL
tr|Q7B8V4|Q7B8V4_CLOBO  LVIIGPSADIIQFECKSFGHEVLNLTNRNGYGSTQYIRFSPDFTFGFEESL
sp|Q45894|BXA2_CLOBO      LVIIGPSADIIQFECKSFGHVDLNLTRNGYGSTQYIRFSPDFTFGFEESL
tr|Q58GH1|Q58GH1_CLOBO  LVIIGPSADIIQFECKSFGHVDLNLTRNGYGSTQYIRFSPDFTFGFEESL
                          *****

sp|P10845|BXA1_CLOBO      EVDTNPLLGAAGKATDPAVTLAHELIHAGHRLYGIAINPNRVFKVNTNAY
tr|Q7B8V4|Q7B8V4_CLOBO  EVDTNPLLGAAGKATDPAVTLAHELIHAGHRLYGIAINPNRVFKVNTNAY
sp|Q45894|BXA2_CLOBO      EVDTNPLLGAAGKATDPAVTLAHELIHAEHRLYGIAINPNRVFKVNTNAY
tr|Q58GH1|Q58GH1_CLOBO  EVDTNPLLGAAGKATDPAVTLAHELIHAEHRLYGIAINPNRVFKVNTNAY
                          *****

sp|P10845|BXA1_CLOBO      YEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYNKFKDIASTLNKA
tr|Q7B8V4|Q7B8V4_CLOBO  YEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYNKFKDIASTLNKA
sp|Q45894|BXA2_CLOBO      YEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYNKFKDIASTLNKA
tr|Q58GH1|Q58GH1_CLOBO  YEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYNKFKDIASTLNKA
                          *****

sp|P10845|BXA1_CLOBO      KSIIGTTASLQYMKNVFKEKYLLSEDTSGKFSVDKLFKDKLYKMLTEIYT
tr|Q7B8V4|Q7B8V4_CLOBO  KSIIGTTASLQYMKNVFKEKYLLSEDTSGKFSVDKLFKDKLYKMLTEIYT
sp|Q45894|BXA2_CLOBO      KSIIGTTASLQYMKNVFKEKYLLSEDTSGKFSVDKLFKDKLYKMLTEIYT
tr|Q58GH1|Q58GH1_CLOBO  KSIIGTTASLQYMKNVFKEKYLLSEDTSGKFSVDKLFKDKLYKMLTEIYT
                          ***

sp|P10845|BXA1_CLOBO      EDNFVKFFKVLNRKTYLNFDKAVFKINIVPKVNYTIYDGFNLNNTNLAAN
tr|Q7B8V4|Q7B8V4_CLOBO  EDNFVKFFKVLNRKTYLNFDKAVFKINIVPKVNYTIYDGFNLNNTNLAAN
sp|Q45894|BXA2_CLOBO      EDNFVNFFKVINRKYTLNFDKAVFRINIVPDENYTIKDGFNKLGANLSTN
tr|Q58GH1|Q58GH1_CLOBO  EDNFVNFFKVINRKYTLNFDKAVFRINIVPDENYTIKDGFNKLGANLSTN
                          *****

sp|P10845|BXA1_CLOBO      FNGQNTTEINNMNFTKLKNFTGLFEFYKLLCVRGIIITSKTKSLDKGYNKAL
tr|Q7B8V4|Q7B8V4_CLOBO  FNGQNTTEINNMNFTKLKNFTGLFEFYKLLCVRGIIITSKTKSLDKGYNKAL
sp|Q45894|BXA2_CLOBO      FNGQNTTEINSRNFTRLKNFTGLFEFYKLLCVRGIIIPFKTKSLDEGYNKAL
tr|Q58GH1|Q58GH1_CLOBO  FNGQNTTEINSRNFTRLKNFTGLFEFYKLLCVRGIIIPFKTKSLDEGYNKAL
                          *****

sp|P10845|BXA1_CLOBO      NDLCIKVNNWDLFFSPSEDNFTNDLNKGEEITSNTNIEAAEENISLDLIQ
tr|Q7B8V4|Q7B8V4_CLOBO  NDLCIKVNNWDLFFSPSEDNFTNDLNKGEEITSNTNIEAAEENISLDLIQ
sp|Q45894|BXA2_CLOBO      NDLCIKVNNWDLFFSPSEDNFTNDLDKVEEITADTNIEAAEENISLDLIQ

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tr Q58GH1 Q58GH1_CLOBO	NDLCIKVNNDLFFSPSEDNFTNDLDKVEEITADTNIEAAEENISLDLIQ *****.* ****.******
sp P10845 BXA1_CLOBO	QYYLTFNFDNEPENISIE NLSSDIIGQLELMPNIERFPNGKKYELDKYTM
tr Q7B8V4 Q7B8V4_CLOBO	QYYLTFNFDNEPENISIE NLSSDIIGQLELMPNIERFPNGKKYELDKYTM
sp Q45894 BXA2_CLOBO	QYYLTFDFDNEPENISIE NLSSDIIGQLEPMPNIERFPNGKKYELDKYTM
tr Q58GH1 Q58GH1_CLOBO	QYYLTFDFDNEPENISIE NLSSDIIGQLEPMPNIERFPNGKKYELDKYTM *****:***** *****
sp P10845 BXA1_CLOBO	FHYLRAQEFEGHKSRIALTNSVNEALLNPSRVYTFSSDYVKKVKNKATEA
tr Q7B8V4 Q7B8V4_CLOBO	FHYLRAQEFEGHKSRIALTNSVNEALLNPSRVYTFSSDYVKKVKNKATEA
sp Q45894 BXA2_CLOBO	FHYLRAQEFEGHGSRIILTNSAEEALLKPNVAYTFSSKYVKKINKAVEA
tr Q58GH1 Q58GH1_CLOBO	FHYLRAQEFEGHGSRIILTNSAEEALLKPNVAYTFSSKYVKKINKAVEA *****.* ** *. :****.*. .*****.* **.* **
sp P10845 BXA1_CLOBO	AMFLGWVEQLVYDFTDETSEVSTTDKIADITIIIPYIGPALNIGNMLYKD
tr Q7B8V4 Q7B8V4_CLOBO	AMFLGWVEQLVYDFTDETSEVSTTDKIADITIIIPYIGPALNIGNMLYKD
sp Q45894 BXA2_CLOBO	FMFLNWAEELVYDFTDETNEVTTMDKIADITIIIPYIGPALNIGNMLSKG
tr Q58GH1 Q58GH1_CLOBO	FMFLNWAEELVYDFTDETNEVTTMDKIADITIIIPYIGPALNIGNMLSKG ***.*.*:*****.*.* *****:***** *
sp P10845 BXA1_CLOBO	DFVGALIFSGAVILLEFIPEIAIPVLGTFALVSYIANKVLTQVOTIDNALS
tr Q7B8V4 Q7B8V4_CLOBO	DFVGALIFSGAVILLEFIPEIAIPVLGTFALVSYIANKVLTQVOTIDNALS
sp Q45894 BXA2_CLOBO	EFVEAIIFTGVVAMLEFIPEYALPVFGTFAIVSYIANKVLTQVOTINNALS
tr Q58GH1 Q58GH1_CLOBO	EFVEAIIFTGVVAMLEFIPEYALPVFGTFAIVSYIANKVLTQVOTINNALS :** *:**.* * :***** *:***:****:*****:****
sp P10845 BXA1_CLOBO	KRNEKWDEVYKYIVTNWLAKVNTQIDLIRKKMKEALENQAEATKAIINYQ
tr Q7B8V4 Q7B8V4_CLOBO	KRNEKWDEVYKYIVTNWLAKVNTQIDLIRKKMKEALENQAEATKAIINYQ
sp Q45894 BXA2_CLOBO	KRNEKWDEVYKYIVTNWLAKVNTQIDLIREKMKKALENQAEATKAIINYQ
tr Q58GH1 Q58GH1_CLOBO	KRNEKWDEVYKYIVTNWLAKVNTQIDLIREKMKKALENQAEATKAIINYQ ***** *****:***:*****
sp P10845 BXA1_CLOBO	YNQYTEEEKNNINFNIDDLSSKLNESINKAMININKFLNQCSVSYLMNSM
tr Q7B8V4 Q7B8V4_CLOBO	YNQYTEEEKNNINFNIDDLSSKLNESINKAMININKFLNQCSVSYLMNSM
sp Q45894 BXA2_CLOBO	YNQYTEEEKNNINFNIDDLSSKLNESINSAMININKFLDQCSVSYLMNSM
tr Q58GH1 Q58GH1_CLOBO	YNQYTEEEKNNINFNIDDLSSKLNESINSAMININKFLDQCSVSYLMNSM *****:*****:*****
sp P10845 BXA1_CLOBO	IPYGVKRLDFDASLKDALLKYIYDNRGTLIGQVDRCLKDKVNNTLSTDIP
tr Q7B8V4 Q7B8V4_CLOBO	IPYGVKRLDFDASLKDALLKYIYDNRGTLIGQVDRCLKDKVNNTLSTDIP
sp Q45894 BXA2_CLOBO	IPYAVKRLKDFDASVRDVLLKYIYDNRGTLVLQVDRCLKDEVNNTLSADIP
tr Q58GH1 Q58GH1_CLOBO	IPYAVKRLKDFDASVRDVLLKYIYDNRGTLVLQVDRCLKDEVNNTLSADIP ***.***.*:*****:.* *****: *****:*****:***
sp P10845 BXA1_CLOBO	FQLSKYVDNQRLSLSTFTEYIKNIINTSILNLRYESNHLIDLTRYASKINI
tr Q7B8V4 Q7B8V4_CLOBO	FQLSKYVDNQRLSLSTFTEYIKNIINTSILNLRYESNHLIDLTRYASKINI
sp Q45894 BXA2_CLOBO	FQLSKYVDNKKLLSTFTEYIKNIVNTSILSIVYKKDDLIDLTRYGAKINI
tr Q58GH1 Q58GH1_CLOBO	FQLSKYVDNKKLLSTFTEYIKNIVNTSILSIVYKKDDLIDLTRYGAKINI *****:*****:*****: *.:.*****:****
sp P10845 BXA1_CLOBO	GSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVNSMYENFSTSFWIRIP
tr Q7B8V4 Q7B8V4_CLOBO	GSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVNSMYENFSTSFWIRIP
sp Q45894 BXA2_CLOBO	GDRVYYDSIDKNQIKLINLESSTIEVILKNAIVNSMYENFSTSFWIKIP
tr Q58GH1 Q58GH1_CLOBO	GDRVYYDSIDKNQIKLINLESSTIEVILKNAIVNSMYENFSTSFWIKIP *.:* :*.*****:*.*****.*****:*****:***
sp P10845 BXA1_CLOBO	KYFNSISLNNEYTIINC MENSGWKVSLNYGEIIWTLQDTQEIKQRVVFK
tr Q7B8V4 Q7B8V4_CLOBO	KYFNSISLNNEYTIINC MENSGWKVSLNYGEIIWTLQDTQEIKQRVVFK
sp Q45894 BXA2_CLOBO	KYFSKINLNNEYTIINCIENSGWKVSLNYGEIIWTLQDNKQNIQRVVFK

tr	Q58GH1	Q58GH1_CLOBO	KYFSKINLNNYEYTIINCIENNSGWKVSLNYGEIIWTLQDNKQNIQRVVFK ***. *.*****:*****.***
sp	P10845	BXA1_CLOBO	YSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHAS
tr	Q7B8V4	Q7B8V4_CLOBO	YSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHAS
sp	Q45894	BXA2_CLOBO	YSQMVNISDYINRWIFVTITNNRLTKSKIYINGRLIDQKPISNLGNIHAS
tr	Q58GH1	Q58GH1_CLOBO	YSQMVNISDYINRWIFVTITNNRLTKSKIYINGRLIDQKPISNLGNIHAS ****:*****.***:*****
sp	P10845	BXA1_CLOBO	NNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNISGILKDF
tr	Q7B8V4	Q7B8V4_CLOBO	NNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSNISGILKDF
sp	Q45894	BXA2_CLOBO	NKIMFKLDGCRDPRRYIMIKYFNLFDKELNEKEIKDLYDSQSNISGILKDF
tr	Q58GH1	Q58GH1_CLOBO	NKIMFKLDGCRDPRRYIMIKYFNLFDKELNEKEIKDLYDSQSNISGILKDF *:*****.***:*****
sp	P10845	BXA1_CLOBO	WGDYLQYDKPYMYMLNLYDPNKYVDVNNVGIRGYMYLKGRGSMVTNNIYL
tr	Q7B8V4	Q7B8V4_CLOBO	WGDYLQYDKPYMYMLNLYDPNKYVDVNNVGIRGYMYLKGRGSMVTNNIYL
sp	Q45894	BXA2_CLOBO	WGNYLQYDKPYMYMLNLYDPNKYVDVNNIGIRGYMYLKGRGSMVTNNIYL
tr	Q58GH1	Q58GH1_CLOBO	WGNYLQYDKPYMYMLNLYDPNKYVDVNNIGIRGYMYLKGRGSMVTNNIYL **.:*****:*****:*****:*****
sp	P10845	BXA1_CLOBO	NSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQA
tr	Q7B8V4	Q7B8V4_CLOBO	NSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQA
sp	Q45894	BXA2_CLOBO	NSTLYEGTKFIIKKYASGNEDNIVRNNDRVYINVVVKNKEYRLATNASQA
tr	Q58GH1	Q58GH1_CLOBO	NSTLYEGTKFIIKKYASGNEDNIVRNNDRVYINVVVKNKEYRLATNASQA **.:**.:*****:*****:*****
sp	P10845	BXA1_CLOBO	GVEKILSALEIPDVGNLSQVVMKSKNDQGITNKCKMNLQDNNGNDIGFI
tr	Q7B8V4	Q7B8V4_CLOBO	GVEKILSALEIPDVGNLSQVVMKSKNDQGITNKCKMNLQDNNGNDIGFI
sp	Q45894	BXA2_CLOBO	GVEKILSALEIPDVGNLSQVVMKSKDDQGIRNKCKMNLQDNNGNDIGFI
tr	Q58GH1	Q58GH1_CLOBO	GVEKILSALEIPDVGNLSQVVMKSKDDQGIRNKCKMNLQDNNGNDIGFI *****:*****:*****
sp	P10845	BXA1_CLOBO	GFHQFNNAIKLVASNWYNRQIERSSRTLGCSEFIPVDDGWGERPL
tr	Q7B8V4	Q7B8V4_CLOBO	GFHQFNNAIKLVASNWYNRQIERSSRTLGCSEFIPVDDGWGERPL
sp	Q45894	BXA2_CLOBO	GFHLYDNIAKLVASNWYNRQVGKASRTFGCSEFIPVDDGWGESL
tr	Q58GH1	Q58GH1_CLOBO	GFHLYDNIAKLVASNWYNRQVGKASRTFGCSEFIPVDDGWGESL *** :.:*****: :.:***:***** *

FileUp

MSF: 1296 Type: P Check: 8703 ..

Name: sp|P10845|BXA1_CLOBO oo Len: 1296 Check: 7638 Weight: 0.100
 Name: tr|Q7B8V4|Q7B8V4_CLOBO oo Len: 1296 Check: 7102 Weight: 0.100
 Name: sp|Q45894|BXA2_CLOBO oo Len: 1296 Check: 1966 Weight: 0.100
 Name: tr|Q58GH1|Q58GH1_CLOBO oo Len: 1296 Check: 1997 Weight: 0.100

//

sp P10845 BXA1_CLOBO	.PFVNKQFNY	KDPVNGVDIA	YIKIPNVGQM	QPVKAFKIHN	KIWWIPERDT
tr Q7B8V4 Q7B8V4_CLOBO	MPFVNKQFNY	KDPVNGVDIA	YIKIPNAGQM	QPVKAFKIHN	KIWWIPERDT
sp Q45894 BXA2_CLOBO	.PFVNKQFNY	KDPVNGVDIA	YIKIPNAGQM	QPVKAFKIHN	KIWWIPERDT
tr Q58GH1 Q58GH1_CLOBO	MPFVNKQFNY	KDPVNGVDIA	YIKIPNAGQM	QPVKAFKIHN	KIWWIPERDT

sp P10845 BXA1_CLOBO	FTNPEEGDLN	PPPEAKQVPV	SYDSTYLST	DNEKDNLYKG	VTKLFERIYS
tr Q7B8V4 Q7B8V4_CLOBO	FTNPEEGDLN	PPPEAKQVPV	SYDSTYLST	DNEKDNLYKG	VTKLFERIYS
sp Q45894 BXA2_CLOBO	FTNPEEGDLN	PPPEAKQVPV	SYDSTYLST	DNEKDNLYKG	VTKLFERIYS
tr Q58GH1 Q58GH1_CLOBO	FTNPEEGDLN	PPPEAKQVPV	SYDSTYLST	DNEKDNLYKG	VTKLFERIYS

sp P10845 BXA1_CLOBO	TDLGRMLLTS	IVRGIPFWGG	STIDTELKVI	DTNCINVIQP	DGSYRSEELN
tr Q7B8V4 Q7B8V4_CLOBO	TDLGRMLLTS	IVRGIPFWGG	STIDTELKVI	DTNCINVIQP	DGSYRSEELN
sp Q45894 BXA2_CLOBO	TDLGRMLLTS	IVRGIPFWGG	STIDTELKVI	DTNCINVIQP	DGSYRSEELN
tr Q58GH1 Q58GH1_CLOBO	TDLGRMLLTS	IVRGIPFWGG	STIDTELKVI	DTNCINVIQP	DGSYRSEELN

sp P10845 BXA1_CLOBO	LVIIGPSADI	IQFECKSFGE	EVLNLTRNGY	GSTQYIRFSP	DFTFGFEESL
tr Q7B8V4 Q7B8V4_CLOBO	LVIIGPSADI	IQFECKSFGE	EVLNLTRNGY	GSTQYIRFSP	DFTFGFEESL
sp Q45894 BXA2_CLOBO	LVIIGPSADI	IQFECKSFGE	DVLNLTRNGY	GSTQYIRFSP	DFTFGFEESL
tr Q58GH1 Q58GH1_CLOBO	LVIIGPSADI	IQFECKSFGE	DVLNLTRNGY	GSTQYIRFSP	DFTFGFEESL

sp P10845 BXA1_CLOBO	EVDTNPLLGA	GKFATDPAVT	LAHELIHAGH	RLYGIAINPN	RVFKVNTNAY
tr Q7B8V4 Q7B8V4_CLOBO	EVDTNPLLGA	GKFATDPAVT	LAHELIHAGH	RLYGIAINPN	RVFKVNTNAY
sp Q45894 BXA2_CLOBO	EVDTNPLLGA	GKFATDPAVT	LAHELIHAEH	RLYGIAINPN	RVFKVNTNAY
tr Q58GH1 Q58GH1_CLOBO	EVDTNPLLGA	GKFATDPAVT	LAHELIHAEH	RLYGIAINPN	RVFKVNTNAY

sp P10845 BXA1_CLOBO	YEMSGLEVSF	EELRTFGGHD	AKFIDSLQEN	EFRLYYYNKF	KDIASLTNKA
tr Q7B8V4 Q7B8V4_CLOBO	YEMSGLEVSF	EELRTFGGHD	AKFIDSLQEN	EFRLYYYNKF	KDIASLTNKA
sp Q45894 BXA2_CLOBO	YEMSGLEVSF	EELRTFGGHD	AKFIDSLQEN	EFRLYYYNKF	KDVASTLNKA
tr Q58GH1 Q58GH1_CLOBO	YEMSGLEVSF	EELRTFGGHD	AKFIDSLQEN	EFRLYYYNKF	KDVASTLNKA

sp P10845 BXA1_CLOBO	KSIVGTTASL	QYMKNVFKEK	YLLSEDTSKG	FSVDKLKFDK	LYKMLTEIYT
tr Q7B8V4 Q7B8V4_CLOBO	KSIVGTTASL	QYMKNVFKEK	YLLSEDTSKG	FSVDKLKFDK	LYKMLTEIYT
sp Q45894 BXA2_CLOBO	KSIIGTTASL	QYMKNVFKEK	YLLSEDTSKG	FSVDKLKFDK	LYKMLTEIYT
tr Q58GH1 Q58GH1_CLOBO	KSIIGTTASL	QYMKNVFKEK	YLLSEDTSKG	FSVDKLKFDK	LYKMLTEIYT

sp P10845 BXA1_CLOBO	EDNFVKFFKV	LNRKTYLNFD	KAVFKINIVP	KVNYTIYDGF	NLRNTNLAAN
tr Q7B8V4 Q7B8V4_CLOBO	EDNFVKFFKV	LNRKTYLNFD	KAVFKINIVP	KVNYTIYDGF	NLRNTNLAAN
sp Q45894 BXA2_CLOBO	EDNFVNFFKV	INRKTYLNFD	KAVFRINIVP	DENYTIKDG	NLKGANLSTN

tr Q58GH1 Q58GH1_CLOBO	EDNFVNFFKV INRKTYLNFD KAVFRINIVP DENYTIKDGf NLKGANLSTN
sp P10845 BXA1_CLOBO	FNGQNTTEINN MNFTKLKNFT GLFEFYKLLC VRGIITSKTK SLDKGYNKAL
tr Q7B8V4 Q7B8V4_CLOBO	FNGQNTTEINN MNFTKLKNFT GLFEFYKLLC VRGIITSKTK SLDKGYNKAL
sp Q45894 BXA2_CLOBO	FNGQNTTEINS RNFTRLKNFT GLFEFYKLLC VRGIIPFKTK SLDEGYNKAL
tr Q58GH1 Q58GH1_CLOBO	FNGQNTTEINS RNFTRLKNFT GLFEFYKLLC VRGIIPFKTK SLDEGYNKAL
sp P10845 BXA1_CLOBO	NDLCIKVNNW DLFFSPSEDN FTNDLNKGEE ITSdTNIeAA EENISLDLIQ
tr Q7B8V4 Q7B8V4_CLOBO	NDLCIKVNNW DLFFSPSEDN FTNDLNKGEE ITSdTNIeAA EENISLDLIQ
sp Q45894 BXA2_CLOBO	NDLCIKVNNW DLFFSPSEDN FTNDLDKVEE ITADTNIeAA EENISLDLIQ
tr Q58GH1 Q58GH1_CLOBO	NDLCIKVNNW DLFFSPSEDN FTNDLDKVEE ITADTNIeAA EENISLDLIQ
sp P10845 BXA1_CLOBO	QYYLTFNFDN EPENISIEENL SSDIIGQLEL MPNIERFPNG KKYELDKYTM
tr Q7B8V4 Q7B8V4_CLOBO	QYYLTFNFDN EPENISIEENL SSDIIGQLEL MPNIERFPNG KKYELDKYTM
sp Q45894 BXA2_CLOBO	QYYLTFDFDN EPENISIEENL SSDIIGQLEP MPNIERFPNG KKYELDKYTM
tr Q58GH1 Q58GH1_CLOBO	QYYLTFDFDN EPENISIEENL SSDIIGQLEP MPNIERFPNG KKYELDKYTM
sp P10845 BXA1_CLOBO	FHYLRAQEFf HGKSRIALTn SVNEALLNPS RVYTFfSSDY VKKVNKATEA
tr Q7B8V4 Q7B8V4_CLOBO	FHYLRAQEFf HGKSRIALTn SVNEALLNPS RVYTFfSSDY VKKVNKATEA
sp Q45894 BXA2_CLOBO	FHYLRAQEFf HGDSRIILTn SAEeALLKPN VAYTFfSSKY VKKINKAVEA
tr Q58GH1 Q58GH1_CLOBO	FHYLRAQEFf HGDSRIILTn SAEeALLKPN VAYTFfSSKY VKKINKAVEA
sp P10845 BXA1_CLOBO	AMFLGWVEQL VYDfTDEtSE VSTTDKIADI TIIPYIGPA LNIGNMLYKD
tr Q7B8V4 Q7B8V4_CLOBO	AMFLGWVEQL VYDfTDEtSE VSTTDKIADI TIIPYIGPA LNIGNMLYKD
sp Q45894 BXA2_CLOBO	FMFLNWAEEL VYDfTDEtNE VTTMDKIADI TIIVPYIGPA LNIGNMLSKG
tr Q58GH1 Q58GH1_CLOBO	FMFLNWAEEL VYDfTDEtNE VTTMDKIADI TIIVPYIGPA LNIGNMLSKG
sp P10845 BXA1_CLOBO	DFVGALIFSG AVILLEFIPE IAIPVLGTfA LVSYIANKVL TVQTIDNALS
tr Q7B8V4 Q7B8V4_CLOBO	DFVGALIFSG AVILLEFIPE IAIPVLGTfA LVSYIANKVL TVQTIDNALS
sp Q45894 BXA2_CLOBO	EFVEAIIFTG VVAMLEFIPE YALPVFGTfA IVSYIANKVL TVQTINNALS
tr Q58GH1 Q58GH1_CLOBO	EFVEAIIFTG VVAMLEFIPE YALPVFGTfA IVSYIANKVL TVQTINNALS
sp P10845 BXA1_CLOBO	KRNEKWDEVY KYIVTNWLAK VNTQIDLIRK KMKEALENQA EATKAiINYQ
tr Q7B8V4 Q7B8V4_CLOBO	KRNEKWDEVY KYIVTNWLAK VNTQIDLIRK KMKEALENQA EATKAiINYQ
sp Q45894 BXA2_CLOBO	KRNEKWDEVY KYTVTNWLAK VNTQIDLIRE KMKKALENQA EATKAiINYQ
tr Q58GH1 Q58GH1_CLOBO	KRNEKWDEVY KYTVTNWLAK VNTQIDLIRE KMKKALENQA EATKAiINYQ
sp P10845 BXA1_CLOBO	YNQYTEEEKN NINFNIDDLs SKLNESINKA MININKFLNq CSVSYLMNSM
tr Q7B8V4 Q7B8V4_CLOBO	YNQYTEEEKN NINFNIDDLs SKLNESINKA MININKFLNq CSVSYLMNSM
sp Q45894 BXA2_CLOBO	YNQYTEEEKN NINFNIDDLs SKLNESINSA MININKFLDQ CSVSYLMNSM
tr Q58GH1 Q58GH1_CLOBO	YNQYTEEEKN NINFNIDDLs SKLNESINSA MININKFLDQ CSVSYLMNSM
sp P10845 BXA1_CLOBO	IPYGVKRLed FDASLKDALL KYIYDNRGTL IGQVDRlKDK VNNTLSTDiP
tr Q7B8V4 Q7B8V4_CLOBO	IPYGVKRLed FDASLKDALL KYIYDNRGTL IGQVDRlKDK VNNTLSTDiP
sp Q45894 BXA2_CLOBO	IPYAVKRLKd FDASVRDVLl KYIYDNRGTL VLQVDRlKDE VNNTLSADiP
tr Q58GH1 Q58GH1_CLOBO	IPYAVKRLKd FDASVRDVLl KYIYDNRGTL VLQVDRlKDE VNNTLSADiP
sp P10845 BXA1_CLOBO	FQLSKYVDNq RLLSTfTEYI KNIINTSiLN LRYESNHLID LSRyASKINI
tr Q7B8V4 Q7B8V4_CLOBO	FQLSKYVDNq RLLSTfTEYI KNIINTSiLN LRYESNHLID LSRyASKINI
sp Q45894 BXA2_CLOBO	FQLSKYVDNK KLLSTfTEYI KNIVNTSiLS IYVKKDDLID LSRyGAKINI

tr Q58GH1 Q58GH1_CLOBO	FQLSKYVDNK KLLSTFTEYI KNIVNTSILS IVYKKDDLID LSRYGAKINI
sp P10845 BXA1_CLOBO	GSKVNFDPID KNQIQLFNLE SSKIEVILKN AIVYNSMYEN FSTSFWIRIP
tr Q7B8V4 Q7B8V4_CLOBO	GSKVNFDPID KNQIQLFNLE SSKIEVILKN AIVYNSMYEN FSTSFWIRIP
sp Q45894 BXA2_CLOBO	GDRVYYSID KNQIKLINLE SSTIEVILKN AIVYNSMYEN FSTSFWIKIP
tr Q58GH1 Q58GH1_CLOBO	GDRVYYSID KNQIKLINLE SSTIEVILKN AIVYNSMYEN FSTSFWIKIP
sp P10845 BXA1_CLOBO	KYFNSISLNN EYTIINCMEN NSGWKVSILNY GEIIWTLQDT QEIKQRVVFK
tr Q7B8V4 Q7B8V4_CLOBO	KYFNSISLNN EYTIINCMEN NSGWKVSILNY GEIIWTLQDT QEIKQRVVFK
sp Q45894 BXA2_CLOBO	KYFSKINLNN EYTIINCIEN NSGWKVSILNY GEIIWTLQDN KQNIQRVVFK
tr Q58GH1 Q58GH1_CLOBO	KYFSKINLNN EYTIINCIEN NSGWKVSILNY GEIIWTLQDN KQNIQRVVFK
sp P10845 BXA1_CLOBO	YSQMINISDY INRWIFVTIT NNRLNNSKIY INGRILIDQKP ISNLGNIHAS
tr Q7B8V4 Q7B8V4_CLOBO	YSQMINISDY INRWIFVTIT NNRLNNSKIY INGRILIDQKP ISNLGNIHAS
sp Q45894 BXA2_CLOBO	YSQMVNISDY INRWIFVTIT NNRLTKSKIY INGRILIDQKP ISNLGNIHAS
tr Q58GH1 Q58GH1_CLOBO	YSQMVNISDY INRWIFVTIT NNRLTKSKIY INGRILIDQKP ISNLGNIHAS
sp P10845 BXA1_CLOBO	NNIMFKLDGC RDTHRYIWIK YFNLFDKELN EKEIKDLYDN QNSNGILKDF
tr Q7B8V4 Q7B8V4_CLOBO	NNIMFKLDGC RDTHRYIWIK YFNLFDKELN EKEIKDLYDN QNSNGILKDF
sp Q45894 BXA2_CLOBO	NKIMFKLDGC RDPRRYIMIK YFNLFDKELN EKEIKDLYDS QNSNGILKDF
tr Q58GH1 Q58GH1_CLOBO	NKIMFKLDGC RDPRRYIMIK YFNLFDKELN EKEIKDLYDS QNSNGILKDF
sp P10845 BXA1_CLOBO	WGDYLYQYDKP YYMLNLDPN KYVDVNNVGI RGYMYLKGPR GSVMTTNIYL
tr Q7B8V4 Q7B8V4_CLOBO	WGDYLYQYDKP YYMLNLDPN KYVDVNNVGI RGYMYLKGPR GSVMTTNIYL
sp Q45894 BXA2_CLOBO	WGNLYQYDKP YYMLNLDPN KYVDVNNIGI RGYMYLKGPR GSVVTTNIYL
tr Q58GH1 Q58GH1_CLOBO	WGNLYQYDKP YYMLNLDPN KYVDVNNIGI RGYMYLKGPR GSVVTTNIYL
sp P10845 BXA1_CLOBO	NSSLYRGTKF IIKKYASGNK DNIVRNNDRV YINVVVKKE YRLATNASQA
tr Q7B8V4 Q7B8V4_CLOBO	NSSLYRGTKF IIKKYASGNK DNIVRNNDRV YINVVVKKE YRLATNASQA
sp Q45894 BXA2_CLOBO	NSTLYEGTKF IIKKYASGNE DNIVRNNDRV YINVVVKKE YRLATNASQA
tr Q58GH1 Q58GH1_CLOBO	NSTLYEGTKF IIKKYASGNE DNIVRNNDRV YINVVVKKE YRLATNASQA
sp P10845 BXA1_CLOBO	GVEKILSALE IPDVGNLSQV VVMKSKNDQG ITNKCKMNLQ DNNGNDIGFI
tr Q7B8V4 Q7B8V4_CLOBO	GVEKILSALE IPDVGNLSQV VVMKSKNDQG ITNKCKMNLQ DNNGNDIGFI
sp Q45894 BXA2_CLOBO	GVEKILSALE IPDVGNLSQV VVMKSKDDQG IRNKCKMNLQ DNNGNDIGFI
tr Q58GH1 Q58GH1_CLOBO	GVEKILSALE IPDVGNLSQV VVMKSKDDQG IRNKCKMNLQ DNNGNDIGFI
sp P10845 BXA1_CLOBO	GFHQFNNAK LVSANWYNRQ IERSRTLGC SWEFIPVDDG WGERPL
tr Q7B8V4 Q7B8V4_CLOBO	GFHQFNNAK LVSANWYNRQ IERSRTLGC SWEFIPVDDG WGERPL
sp Q45894 BXA2_CLOBO	GFHLYDNIAK LVSANWYNRQ VGKASRTFGC SWEFIPVDDG WGESL
tr Q58GH1 Q58GH1_CLOBO	GFHLYDNIAK LVSANWYNRQ VGKASRTFGC SWEFIPVDDG WGESL

sp P10845 Botulinum neurotoxin type A precursor (EC 3.4.24.69) 1295
 BXA1_CLOBO (BoNT/A) AA
 (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin align
 A light-chain; Botulinum neurotoxin A heavy-chain] [botA]
 [Clostridium botulinum]

Score = 868 bits (2243), Expect = 0.0
 Identities = 423/423 (100%), Positives = 423/423 (100%)

Query: 1 INTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
 INTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
 Sbjct: 873 INTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 932

Query: 61 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI 120
 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI
 Sbjct: 933 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI 992

Query: 121 KQRVVFKEYSQMINISDYINRWIFVTITNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
 KQRVVFKEYSQMINISDYINRWIFVTITNRLNNSKIYINGRLIDQKPISNLGNIHASNNI
 Sbjct: 993 KQRVVFKEYSQMINISDYINRWIFVTITNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 1052

Query: 181 MFKLDGCRDTHRYIWI KYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYDKPYYM 240
 MFKLDGCRDTHRYIWI KYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYDKPYYM
 Sbjct: 1053 MFKLDGCRDTHRYIWI KYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYDKPYYM 1112

Query: 241 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI 300
 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI
 Sbjct: 1113 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI 1172

Query: 301 VRNNDRVYINVVVKNKYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKNDQGITN 360
 VRNNDRVYINVVVKNKYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKNDQGITN
 Sbjct: 1173 VRNNDRVYINVVVKNKYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKNDQGITN 1232

Query: 361 KCKMNLQDNNNDIGFIGFHQFNNAKLVASNWNRYRQIERSSRTLGCSEWFIPVDDGWGE 420
 KCKMNLQDNNNDIGFIGFHQFNNAKLVASNWNRYRQIERSSRTLGCSEWFIPVDDGWGE
 Sbjct: 1233 KCKMNLQDNNNDIGFIGFHQFNNAKLVASNWNRYRQIERSSRTLGCSEWFIPVDDGWGE 1292

Query: 421 RPL 423
 RPL
 Sbjct: 1293 RPL 1295

tr Q7B8V4 BoNT/A (Neurotoxin BoNT) [bont/a] [Clostridium 1296
 Q7B8V4_CLOBO botulinum] AA
 align

Score = 868 bits (2243), Expect = 0.0
 Identities = 423/423 (100%), Positives = 423/423 (100%)

Query: 1 INTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
 INTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV
 Sbjct: 874 INTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 933

Query: 61 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI 120
 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI
 Sbjct: 934 YNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGEIIWTLQDTQEI 993

Query: 121 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI
 Sbjct: 994 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 1053

Query: 181 MFKLDGCRDTHRYIWIKEYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQDKPYM 240
 MFKLDGCRDTHRYIWIKEYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQDKPYM
 Sbjct: 1054 MFKLDGCRDTHRYIWIKEYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQDKPYM 1113

Query: 241 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI 300
 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI
 Sbjct: 1114 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI 1173

Query: 301 VRNNDRVYINVVVKNEYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKNDQGITN 360
 VRNNDRVYINVVVKNEYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKNDQGITN
 Sbjct: 1174 VRNNDRVYINVVVKNEYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKNDQGITN 1233

Query: 361 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYQIERSSRTLGCSEWEIFVDDGWGE 420
 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYQIERSSRTLGCSEWEIFVDDGWGE
 Sbjct: 1234 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYQIERSSRTLGCSEWEIFVDDGWGE 1293

Query: 421 RPL 423
 RPL
 Sbjct: 1294 RPL 1296

sp Q45894 Botulinum neurotoxin type A precursor (EC 3.4.24.69) 1295
 BXA2_CLOBO (BoNT/A) AA
 (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin align
 A light-chain; Botulinum neurotoxin A heavy-chain] [botA]
 [Clostridium botulinum]

Score = 765 bits (1976), Expect = 0.0
 Identities = 368/423 (86%), Positives = 397/423 (92%)

Query: 1 INTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
 +NTSIL++ Y+ + LIDLRLRY +KINIG +V +D IDKNQI+L NLESS IEVILKNAIV
 Sbjct: 873 VNTSILSIVYKDDIDLRLRYGAKINIGDRVYYSIDKNQIKLINLESSTIEVILKNAIV 932

Query: 61 YNSMYENFSTSFWRIPKYFNSISLNNEYTIINC MENNSGWKVS LNYGEIIWTLQDTQEI 120
 YNSMYENFSTSFWI+IPKYF+ I+LNNEYTIINC+ENNSGWKVS LNYGEIIWTLQD ++
 Sbjct: 933 YNSMYENFSTSFWIKIPKYFSKINLNNEYTIINCIENNSGWKVS LNYGEIIWTLQDNKQN 992

Query: 121 KQRVVFYKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
 QRVVVFYKYSQMINISDYINRWIFVTITNNRL SKIYINGRLIDQKPISNLGNIHASN I
 Sbjct: 993 IQRVVFYKYSQMVNISDYINRWIFVTITNNRLTKSKIYINGRLIDQKPISNLGNIHASNKI 1052

Query: 181 MFKLDGCRDTHRYIWIKEYFNLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQDKPYM 240
 MFKLDGCRD RYI IKYFNLFDKELNEKEIKDLYD+QSN SGILKDFWG+YLQYDKPYM
 Sbjct: 1053 MFKLDGCRDPRRYIMIKYFNLFDKELNEKEIKDLYDSQSN SGILKDFWGNLYLYQDKPYM 1112

Query: 241 LNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNI 300
 LNL+DPNKYVDVNN+GIRGYMYLKGPRGSV+TTNIYLN+LY GTKFIIKKYASGN+DNI
 Sbjct: 1113 LNLDPNKYVDVNNIGIRGYMYLKGPRGSVTTNIYLNSTLYEGTKFIIKKYASGNEDNI 1172

Query: 301 VRNNDRVYINVVVKNEYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSKNDQGITN 360
 VRNNDRVYINVVVKNEYRLATNASQAGVEKILSALEIPDVGNLSQVVMKSK+DQGI N

Sbjct: 1173 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKDDQGIRN 1232

Query: 361 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYRQIERSSRTLGCSEFIPVDDGWGE 420
KCKMNLQDNNNGNDIGFIGFH ++NIAKLVASNWNRYRQ+ ++SRT GCSWEFIPVDDGWGE

Sbjct: 1233 KCKMNLQDNNNGNDIGFIGFHLVDNIAKLVASNWNRYRQVGKASRTFGCSWEFIPVDDGWGE 1292

Query: 421 RPL 423
L

Sbjct: 1293 SSL 1295

tr Q58GH1 Type A2 botulinum neurotoxin [Clostridium botulinum] 1296 AA
Q58GH1_CLOBO

align

Score = 765 bits (1976), Expect = 0.0
Identities = 368/423 (86%), Positives = 397/423 (92%)

Query: 1 INTSILNLRYESNHLIDLRLRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIV 60
+NTSIL++ Y+ + LIDLRLRY +KINIG +V +D IDKNQI+L NLESS IEVILKNAIV

Sbjct: 874 VNTSILSIVYKKDDLIDLRLRYGAKINIGDRVYYSIDKNQIKLINLESSTIEVILKNAIV 933

Query: 61 YNSMYENFSTSFWRIPKYFNSISLNNEYTIINCMENNSGWKVS LN YGEIIWTLQDTQEI 120
YNSMYENFSTSFWRIPKYF+ I+LNNEYTIINC+ENNSGWKVS LN YGEIIWTLQD ++

Sbjct: 934 YNSMYENFSTSFWRIPKYFNSISLNNEYTIINCIENNSGWKVS LN YGEIIWTLQDNKQN 993

Query: 121 KQRVVFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNI 180
QRVVFKYSQMINISDYINRWIFVTITNNRL SKIYINGRLIDQKPISNLGNIHASN I

Sbjct: 994 IQRVVFKYSQMVNISDYINRWIFVTITNNRLTKSKIYINGRLIDQKPISNLGNIHASNKI 1053

Query: 181 MFKL DGC RD THRYIWKYFNLFDKELNEKEIKDLYDQSN SGILKDFWGDYLYQDKPYM 240
MFKL DGC RD RYI IKYFNLFDKELNEKEIKDLYD+QSN SGILKDFWG+YLYQDKPYM

Sbjct: 1054 MFKL DGC RD PRYIMIKYFNLFDKELNEKEIKDLYDQSN SGILKDFWGNLYQDKPYM 1113

Query: 241 LNL YDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIKKYASGNKDNI 300
LNL+DPNKYVDVNN+GIRGYMYLKGPRGSV+TTNIYLN S+LY GTKFIKKYASGN+DNI

Sbjct: 1114 LNL FDPNKYVDVNNIGIRGYMYLKGPRGSVTTNIYLNSTLYEGTKFIKKYASGNEDNI 1173

Query: 301 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITN 360
VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSK+DQGI N

Sbjct: 1174 VRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKDDQGIRN 1233

Query: 361 KCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNRYRQIERSSRTLGCSEFIPVDDGWGE 420
KCKMNLQDNNNGNDIGFIGFH ++NIAKLVASNWNRYRQ+ ++SRT GCSWEFIPVDDGWGE

Sbjct: 1234 KCKMNLQDNNNGNDIGFIGFHLVDNIAKLVASNWNRYRQVGKASRTFGCSWEFIPVDDGWGE 1293

Query: 421 RPL 423
L

Sbjct: 1294 SSL 1296